Sequence Listing

<110> Desnoyers,Luc
Eaton,Dan L.
Goddard,Audrey
Godowski,Paul J.
Gurney,Austin L.
Pan,James
Stewart,Timothy A.
Watanabe,Colin K.
Wood,William I.
Zhang,Zemin

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Asp	Leu	Gly	Pro	Arg	Gly	Glu	Arg	Gly	Gln	His	Gly	Pro	Lys	Gly
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Glu	Lys	Gly	Tyr	Pro	Gly	Ile	Pro	Pro	Glu	Leu	Gln	Ile	Ala	Phe
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Met	Ala	Ser	Leu	Ala	Thr	His	Phe	Ser	Asn	Gln	Asn	Ser	Gly	Ile
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Ile	Phe	Ser	Ser	Val	Glu	Thr	Asn	Ile	Gly	Asn	Phe	Phe	Asp	Val
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155 160 165

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170 175 180

Tyr Leu Met His Asn Gly Asn Thr Val Phe Ser Met Tyr Ser Tyr
185 190 195

Glu Met Lys Gly Lys Ser Asp Thr Ser Ser Asn His Ala Val Leu
200 205 210

Lys Leu Ala Lys Gly Asp Glu Val Trp Leu Arg Met Gly Asn Gly
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Leu	Asp	Gly	Phe	Arg	Ser	Asp	Tyr	Ile	Ser	Asp	Glu	Ala	Leu	Glu
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Ser	Leu	Pro	Gly	Phe	Lys	Glu	Ile	Val	Ser	Arg	Gly	Val	Lys	Val
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Asp	Tyr	Leu	Thr	Pro	Asp	Phe	Pro	Ser	Leu	Ser	Tyr	Pro	Asn	Tyr
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Tyr	Thr	Leu	Met	Thr	Gly	Arg	His	Cys	Glu	Val	His	Gln	Met	Ile
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Gly His His Tyr Gly Pro Ala Ser Pro Gln Arg Lys Asp Ala Leu
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Lys Ala Val Asp Thr Val Leu Lys Tyr Met Thr Lys Trp Ile Gln
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Glu Arg Gly Leu Gln Asp Arg Leu Asn Val Ile Ile Phe Ser Asp
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His Gly Met Thr Asp Ile Phe Trp Met Asp Lys Val Ile Glu Leu
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Asn Lys Tyr Ile Ser Leu Asn Asp Leu Gln Gln Val Lys Asp Arg
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Val Ser Pro Leu Thr Leu Val Ala Asp Glu Gly Trp Phe Ile Thr
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Glu Asn Arg Glu Met Leu Pro Phe Trp Met Asn Ser Thr Gly Arg
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Arg Glu Gly Trp Gln Arg Gly Trp His Gly Tyr Asp Asn Glu Leu
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Met Asp Met Arg Gly Ile Phe Leu Ala Phe Gly Pro Asp Phe Lys
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Ser Asn Phe Arg Ala Ala Pro Ile Arg Ser Val Asp Val Tyr Asn
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Val Met Cys Asn Val Val Gly Ile Thr Pro Leu Pro Asn Asn Gly
                395                 400                 405
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Ser Trp Ser Arg Val Met Cys Met Leu Lys Gly Arg Ala Gly Thr
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35 40 45

Gln Ala Pro Pro His Leu Leu Ala Arg Gly Ala Lys Trp Gly Gln
50 55 60

Ala Leu Pro Val Ala Leu Val Ser Ser Leu Glu Ala Ala Ser His
65 70 75

Arg Gly Arg His Glu Arg Pro Ser Ala Thr Thr Gln Cys Pro Val
80 85 90

Leu Arg Pro Glu Glu Val Leu Glu Ala Asp Thr His Gln Arg Ser
95 100 105

Ile Ser Pro Trp Arg Tyr Arg Val Asp Thr Asp Glu Asp Arg Tyr
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Pro Gln Lys Leu Ala Phe Ala Glu Cys Leu Cys Arg Gly Cys Ile
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Asp Ala Arg Thr Gly Arg Glu Thr Ala Ala Leu Asn Ser Val Arg
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Leu Leu Gln Ser Leu Leu Val Leu Arg Arg Arg Pro Cys Ser Arg
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20 25 30

Phe Gly Gly Cys Ser His Gly Ser Arg Cys Leu Arg Asp Ser Thr
35 40 45

His Cys Val Thr Thr Ala Thr Arg Val Leu Ser Asn Thr Glu Asp
50 55 60

Leu Pro Leu Val Thr Lys Met Cys His Ile Gly Cys Pro Asp Ile
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Pro Ser Leu Gly Leu Gly Pro Tyr Val Ser Ile Ala Cys Cys Gln
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Thr Ser Leu Cys Asn His Asp
95

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<212> DNA
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aaacctcctc aaacatttta cttagaggca aggattgtct aatttcaatt 1900

gtgcaagaca tgtgccttat aattattttt agcttaaaat taaacagatt 1950

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caagagaaag ttgtaactct ctggtcttca tatgtccctg tgctcctttt 2500

aaccaaataa agagttcttg tttctggggg aaaaaaaaaa aaaaaaaaaa 2550

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<210> 18
<211> 273
<212> PRT
<213> Homo Sapien

<400> 18

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				20				25						30
Cys	Phe	Ala	Asp	Phe	Lys	His	Pro	Cys	Tyr	Lys	Met	Ala	Tyr	Phe
				35				40						45
His	Glu	Leu	Ser	Ser	Arg	Val	Ser	Phe	Gln	Glu	Ala	Arg	Leu	Ala
				50				55						60
Cys	Glu	Ser	Glu	Gly	Gly	Val	Leu	Leu	Ser	Leu	Glu	Asn	Glu	Ala
				65				70						75
Glu	Gln	Lys	Leu	Ile	Glu	Ser	Met	Leu	Gln	Asn	Leu	Thr	Lys	Pro
				80				85						90
Gly	Thr	Gly	Ile	Ser	Asp	Gly	Asp	Phe	Trp	Ile	Gly	Leu	Trp	Arg
				95				100						105
Asn	Gly	Asp	Gly	Gln	Thr	Ser	Gly	Ala	Cys	Pro	Asp	Leu	Tyr	Gln
				110				115						120
Trp	Ser	Asp	Gly	Ser	Asn	Ser	Gln	Tyr	Arg	Asn	Trp	Tyr	Thr	Asp
				125				130						135
Glu	Pro	Ser	Cys	Gly	Ser	Glu	Lys	Cys	Val	Val	Met	Tyr	His	Gln
				140				145						150
Pro	Thr	Ala	Asn	Pro	Gly	Leu	Gly	Gly	Pro	Tyr	Leu	Tyr	Gln	Trp
				155				160						165
Asn	Asp	Asp	Arg	Cys	Asn	Met	Lys	His	Asn	Tyr	Ile	Cys	Lys	Tyr

170 175 180

Glu Pro Glu Ile Asn Pro Thr Ala Pro Val Glu Lys Pro Tyr Leu
185 190 195

Thr Asn Gln Pro Gly Asp Thr His Gln Asn Val Val Val Thr Glu
200 205 210

Ala Gly Ile Ile Pro Asn Leu Ile Tyr Val Val Ile Pro Thr Ile
215 220 225

Pro Leu Leu Leu Leu Ile Leu Val Ala Phe Gly Thr Cys Cys Phe
230 235 240

Gln Met Leu His Lys Ser Lys Gly Arg Thr Lys Thr Ser Pro Asn
245 250 255

Gln Ser Thr Leu Trp Ile Ser Lys Ser Thr Arg Lys Glu Ser Gly
260 265 270

Met Glu Val

<210> 19
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 19
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<210> 20
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 20
accacattct gatgggtgtc tcctgg 26

<210> 21
<211> 49
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 21
gggtccctac ctttaccagt ggaatgatga caggtgtaac atgaagcac 49

<210> 22
<211> 3824

<212> DNA
<213> Homo Sapien

<400> 22
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gcgtgaaggg cacagaccgc cttgtgaatg tctttctggg cattccattt 200

gcccagccgc cactgggccc tgaccggttc tcagccccac acccagcaca 250

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cagatcttct ccgtttcaga ggactgcctg gtcctcaacg tctatagccc 400

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aataaatctt gctactgccc aaaa 3824

<210> 23
<211> 571
<212> PRT
<213> Homo Sapien

<400> 23

Met Glu Arg Ala Val Arg Val Glu Ser Gly Val Leu Val Gly Val
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Val Cys Leu Leu Leu Ala Cys Pro Ala Thr Ala Thr Gly Pro Glu
20 25 30

Val Ala Gln Pro Glu Val Asp Thr Thr Leu Gly Arg Val Arg Gly
35 40 45

Arg Gln Val Gly Val Lys Gly Thr Asp Arg Leu Val Asn Val Phe

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                50                  55                  60

Leu Gly Ile Pro Phe Ala Gln Pro Pro Leu Gly Pro Asp Arg Phe
                65                  70                  75

Ser Ala Pro His Pro Ala Gln Pro Trp Glu Gly Val Arg Asp Ala
                80                  85                  90

Ser Thr Ala Pro Pro Met Cys Leu Gln Asp Val Glu Ser Met Asn
                95                 100                 105

Ser Ser Arg Phe Val Leu Asn Gly Lys Gln Gln Ile Phe Ser Val
               110                 115                 120

Ser Glu Asp Cys Leu Val Leu Asn Val Tyr Ser Pro Ala Glu Val
               125                 130                 135

Pro Ala Gly Ser Gly Arg Pro Val Met Val Trp Val His Gly Gly
               140                 145                 150

Ala Leu Ile Thr Gly Ala Ala Thr Ser Tyr Asp Gly Ser Ala Leu
               155                 160                 165

Ala Ala Tyr Gly Asp Val Val Val Val Thr Val Gln Tyr Arg Leu
               170                 175                 180

Gly Val Leu Gly Phe Phe Ser Thr Gly Asp Glu His Ala Pro Gly
               185                 190                 195

Asn Gln Gly Phe Leu Asp Val Val Ala Ala Leu Arg Trp Val Gln
               200                 205                 210

Glu Asn Ile Ala Pro Phe Gly Gly Asp Leu Asn Cys Val Thr Val
               215                 220                 225

Phe Gly Gly Ser Ala Gly Gly Ser Ile Ile Ser Gly Leu Val Leu
               230                 235                 240

Ser Pro Val Ala Ala Gly Leu Phe His Arg Ala Ile Thr Gln Ser
               245                 250                 255

Gly Val Ile Thr Thr Pro Gly Ile Ile Asp Ser His Pro Trp Pro
               260                 265                 270

Leu Ala Gln Lys Ile Ala Asn Thr Leu Ala Cys Ser Ser Ser Ser
               275                 280                 285

Pro Ala Glu Met Val Gln Cys Leu Gln Gln Lys Glu Gly Glu Glu
               290                 295                 300

Leu Val Leu Ser Lys Lys Leu Lys Asn Thr Ile Tyr Pro Leu Thr
               305                 310                 315

Val Asp Gly Thr Val Phe Pro Lys Ser Pro Lys Glu Leu Leu Lys
               320                 325                 330

Glu Lys Pro Phe His Ser Val Pro Phe Leu Met Gly Val Asn Asn
               335                 340                 345
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His Glu Phe Ser Trp Leu Ile Pro Arg Gly Trp Gly Leu Leu Asp
350 355 360

Thr Met Glu Gln Met Ser Arg Glu Asp Met Leu Ala Ile Ser Thr
365 370 375

Pro Val Leu Thr Ser Leu Asp Val Pro Pro Glu Met Met Pro Thr
380 385 390

Val Ile Asp Glu Tyr Leu Gly Ser Asn Ser Asp Ala Gln Ala Lys
395 400 405

Cys Gln Ala Phe Gln Glu Phe Met Gly Asp Val Phe Ile Asn Val
410 415 420

Pro Thr Val Ser Phe Ser Arg Tyr Leu Arg Asp Ser Gly Ser Pro
425 430 435

Val Phe Phe Tyr Glu Phe Gln His Arg Pro Ser Ser Phe Ala Lys
440 445 450

Ile Lys Pro Ala Trp Val Lys Ala Asp His Gly Ala Glu Gly Ala
455 460 465

Phe Val Phe Gly Gly Pro Phe Leu Met Asp Glu Ser Ser Arg Leu
470 475 480

Ala Phe Pro Glu Ala Thr Glu Glu Glu Lys Gln Leu Ser Leu Thr
485 490 495

Met Met Ala Gln Trp Thr His Phe Ala Arg Thr Gly Asp Pro Asn
500 505 510

Ser Lys Ala Leu Pro Pro Trp Pro Gln Phe Asn Gln Ala Glu Gln
515 520 525

Tyr Leu Glu Ile Asn Pro Val Pro Arg Ala Gly Gln Lys Phe Arg
530 535 540

Glu Ala Trp Met Gln Phe Trp Ser Glu Thr Leu Pro Ser Lys Ile
545 550 555

Gln Gln Trp His Gln Lys Gln Lys Asn Arg Lys Ala Gln Glu Asp
560 565 570

Leu

<210> 24
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 24
gcaaagctct gcctccttgg cc 22

<210> 25
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<220>
<223> Synthetic oligonucleotide probe

<400> 25
gggtggactg tgctctaatg gacgc 25

<210> 26
<211> 18
<212> DNA
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<220>
<223> Synthetic oligonucleotide probe

<400> 26
cgtggcactg ggttgatc 18

<210> 27
<211> 45
<212> DNA
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<220>
<223> Synthetic oligonucleotide probe

<400> 27
gatgcagttc tggtcagaga cgctccccag caagatacaa cagtg 45

<210> 28
<211> 1342
<212> DNA
<213> Homo Sapien

<400> 28
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cttctacaac taaaattcct caaacctaaa atcaacagct tttatgcctt 150

tgaagtgaag gatgcaaaag gaagaactgt ttctctggaa aagtataaag 200

gcaaagtttc actagttgta aacgtggcca gtgactgcca actcacagac 250

agaaattact tagggctgaa ggaactgcac aaagagtttg gaccatccca 300

cttcagcgtg ttggcttttc cctgcaatca gtttggagaa tcggagcccc 350

gcccaagcaa ggaagtagaa tcttttgcaa gaaaaaacta cggagtaact 400

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atttagattt cttgttgatt cttcaaagaa ggaaccaagg tggaattttt 500

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ttttttgga gacagtgtct cactctgtca cccaggctgg agtgcagtag 750

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aaagaatcaa catgaaatat attaactact tcctctgacc atactaaaga 950

attcagaata cacagtgacc aatgtgcctc aatatcttat tgttcaactt 1000

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tcactatgta tgtaactgac atatataaat agtcatttat aaatgaccgt 1300

attataacat ttgaaaaagt cttcatcaaa aaaaaaaaaa aa 1342

<210> 29
<211> 209
<212> PRT
<213> Homo Sapien

<400> 29

Met	Glu	Pro	Leu	Ala	Ala	Tyr	Pro	Leu	Lys	Cys	Ser	Gly	Pro	Arg	
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Ala	Lys	Val	Phe	Ala	Val	Leu	Leu	Ser	Ile	Val	Leu	Cys	Thr	Val	
				20				25						30	
Thr	Leu	Phe	Leu	Leu	Gln	Leu	Lys	Phe	Leu	Lys	Pro	Lys	Ile	Asn	
				35				40						45	
Ser	Phe	Tyr	Ala	Phe	Glu	Val	Lys	Asp	Ala	Lys	Gly	Arg	Thr	Val	
				50				55						60	
Ser	Leu	Glu	Lys	Tyr	Lys	Gly	Lys	Val	Ser	Leu	Val	Val	Asn	Val	
				65				70						75	
Ala	Ser	Asp	Cys	Gln	Leu	Thr	Asp	Arg	Asn	Tyr	Leu	Gly	Leu	Lys	
				80				85						90	

Glu Leu His Lys Glu Phe Gly Pro Ser His Phe Ser Val Leu Ala
95 100 105

Phe Pro Cys Asn Gln Phe Gly Glu Ser Glu Pro Arg Pro Ser Lys
110 115 120

Glu Val Glu Ser Phe Ala Arg Lys Asn Tyr Gly Val Thr Phe Pro
125 130 135

Ile Phe His Lys Ile Lys Ile Leu Gly Ser Glu Gly Glu Pro Ala
140 145 150

Phe Arg Phe Leu Val Asp Ser Ser Lys Lys Glu Pro Arg Trp Asn
155 160 165

Phe Trp Lys Tyr Leu Val Asn Pro Glu Gly Gln Val Val Lys Phe
170 175 180

Trp Arg Pro Glu Glu Pro Ile Glu Val Ile Arg Pro Asp Ile Ala
185 190 195

Ala Leu Val Arg Gln Val Ile Ile Lys Lys Lys Glu Asp Leu
200 205

<210> 30
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<223> Synthetic oligonucleotide probe

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<400> 31
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<210> 32
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<220>
<223> Synthetic oligonucleotide probe

<400> 32
taaccagagc tgctatgtca ggcc 24

<210> 33

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<212> DNA
<213> Artificial Sequence

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<223> Synthetic oligonucleotide probe

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<210> 34
<211> 3721
<212> DNA
<213> Homo Sapien

<400> 34
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aaaaaaaaaa aaaaaaaaaa a 3721

<210> 35
<211> 888
<212> PRT
<213> Homo Sapien

<400> 35
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Pro Pro Pro Leu Ser Val Ala Pro Arg Asp Tyr Leu Asn His Tyr
35 40 45

Pro Val Phe Val Gly Ser Gly Pro Gly Arg Leu Thr Pro Ala Glu
50 55 60

Gly Ala Asp Asp Leu Asn Ile Gln Arg Val Leu Arg Val Asn Arg
65 70 75

Thr Leu Phe Ile Gly Asp Arg Asp Asn Leu Tyr Arg Val Glu Leu
80 85 90

Glu Pro Pro Thr Ser Thr Glu Leu Arg Tyr Gln Arg Lys Leu Thr
95 100 105

Trp Arg Ser Asn Pro Ser Asp Ile Asn Val Cys Arg Met Lys Gly
110 115 120

Lys Gln Glu Gly Glu Cys Arg Asn Phe Val Lys Val Leu Leu Leu
125 130 135

Arg Asp Glu Ser Thr Leu Phe Val Cys Gly Ser Asn Ala Phe Asn
140 145 150

Pro Val Cys Ala Asn Tyr Ser Ile Asp Thr Leu Gln Pro Val Gly
155 160 165

Asp Asn Ile Ser Gly Met Ala Arg Cys Pro Tyr Asp Pro Lys His
170 175 180

Ala Asn Val Ala Leu Phe Ser Asp Gly Met Leu Phe Thr Ala Thr
185 190 195

Val Thr Asp Phe Leu Ala Ile Asp Ala Val Ile Tyr Arg Ser Leu
200 205 210

Gly Asp Arg Pro Thr Leu Arg Thr Val Lys His Asp Ser Lys Trp
215 220 225

Phe Lys Glu Pro Tyr Phe Val His Ala Val Glu Trp Gly Ser His
230 235 240

Val Tyr Phe Phe Phe Arg Glu Ile Ala Met Glu Phe Asn Tyr Leu
245 250 255

Glu Lys Val Val Val Ser Arg Val Ala Arg Val Cys Lys Asn Asp
260 265 270

Val Gly Gly Ser Pro Arg Val Leu Glu Lys Gln Trp Thr Ser Phe
275 280 285

Leu Lys Ala Arg Leu Asn Cys Ser Val Pro Gly Asp Ser His Phe
290 295 300

Tyr Phe Asn Val Leu Gln Ala Val Thr Gly Val Val Ser Leu Gly

305 310 315

Gly Arg Pro Val Val Leu Ala Val Phe Ser Thr Pro Ser Asn Ser
320 325 330

Ile Pro Gly Ser Ala Val Cys Ala Phe Asp Leu Thr Gln Val Ala
335 340 345

Ala Val Phe Glu Gly Arg Phe Arg Glu Gln Lys Ser Pro Glu Ser
350 355 360

Ile Trp Thr Pro Val Pro Glu Asp Gln Val Pro Arg Pro Arg Pro
365 370 375

Gly Cys Cys Ala Ala Pro Gly Met Gln Tyr Asn Ala Ser Ser Ala
380 385 390

Leu Pro Asp Asp Ile Leu Asn Phe Val Lys Thr His Pro Leu Met
395 400 405

Asp Glu Ala Val Pro Ser Leu Gly His Ala Pro Trp Ile Leu Arg
410 415 420

Thr Leu Met Arg His Gln Leu Thr Arg Val Ala Val Asp Val Gly
425 430 435

Ala Gly Pro Trp Gly Asn Gln Thr Val Val Phe Leu Gly Ser Glu
440 445 450

Ala Gly Thr Val Leu Lys Phe Leu Val Arg Pro Asn Ala Ser Thr
455 460 465

Ser Gly Thr Ser Gly Leu Ser Val Phe Leu Glu Glu Phe Glu Thr
470 475 480

Tyr Arg Pro Asp Arg Cys Gly Arg Pro Gly Gly Gly Glu Thr Gly
485 490 495

Gln Arg Leu Leu Ser Leu Glu Leu Asp Ala Ala Ser Gly Gly Leu
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Leu Ala Ala Phe Pro Arg Cys Val Val Arg Val Pro Val Ala Arg
515 520 525

Cys Gln Gln Tyr Ser Gly Cys Met Lys Asn Cys Ile Gly Ser Gln
530 535 540

Asp Pro Tyr Cys Gly Trp Ala Pro Asp Gly Ser Cys Ile Phe Leu
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Ser Pro Gly Thr Arg Ala Ala Phe Glu Gln Asp Val Ser Gly Ala
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Ser Thr Ser Gly Leu Gly Asp Cys Thr Gly Leu Leu Arg Ala Ser
575 580 585

Leu Ser Glu Asp Arg Ala Gly Leu Val Ser Val Asn Leu Leu Val
590 595 600

Thr Ser Ser Val Ala Ala Phe Val Val Gly Ala Val Val Ser Gly
605 610 615

Phe Ser Val Gly Trp Phe Val Gly Leu Arg Glu Arg Arg Glu Leu
620 625 630

Ala Arg Arg Lys Asp Lys Glu Ala Ile Leu Ala His Gly Ala Gly
635 640 645

Glu Ala Val Leu Ser Val Ser Arg Leu Gly Glu Arg Arg Ala Gln
650 655 660

Gly Pro Gly Gly Arg Gly Gly Gly Gly Gly Gly Gly Ala Gly Val
665 670 675

Pro Pro Glu Ala Leu Leu Ala Pro Leu Met Gln Asn Gly Trp Ala
680 685 690

Lys Ala Thr Leu Leu Gln Gly Gly Pro His Asp Leu Asp Ser Gly
695 700 705

Leu Leu Pro Thr Pro Glu Gln Thr Pro Leu Pro Gln Lys Arg Leu
710 715 720

Pro Thr Pro His Pro His Pro His Ala Leu Gly Pro Arg Ala Trp
725 730 735

Asp His Gly His Pro Leu Leu Pro Ala Ser Ala Ser Ser Ser Leu
740 745 750

Leu Leu Leu Ala Pro Ala Arg Ala Pro Glu Gln Pro Pro Ala Pro
755 760 765

Gly Glu Pro Thr Pro Asp Gly Arg Leu Tyr Ala Ala Arg Pro Gly
770 775 780

Arg Ala Ser His Gly Asp Phe Pro Leu Thr Pro His Ala Ser Pro
785 790 795

Asp Arg Arg Arg Val Val Ser Ala Pro Thr Gly Pro Leu Asp Pro
800 805 810

Ala Ser Ala Ala Asp Gly Leu Pro Arg Pro Trp Ser Pro Pro Pro
815 820 825

Thr Gly Ser Leu Arg Arg Pro Leu Gly Pro His Ala Pro Pro Ala
830 835 840

Ala Thr Leu Arg Arg Thr His Thr Phe Asn Ser Gly Glu Ala Arg
845 850 855

Pro Gly Asp Arg His Arg Gly Cys His Ala Arg Pro Gly Thr Asp
860 865 870

Leu Ala His Leu Leu Pro Tyr Gly Gly Ala Asp Arg Thr Ala Pro
875 880 885

Pro Val Pro

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<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 36
gaggacctac cggccggaca g 21

<210> 37
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 37
atacaccccg agtactgctg gcag 24

<210> 38
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 38
agacagggca gcggctgctg agcttggagc tggacgcagc tt 42

<210> 39
<211> 2014
<212> DNA
<213> Homo Sapien

<400> 39
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ggccgggaca gcagaacgcc aggggaccct cacctgggcg cgccggggca 100

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gccgggcggc aacctttgca gtcgcgttgg ctgctgcgat cggccggcgg 200

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ctactttatt gcttctttct ggcgacagtt ccagcactcg ccgagaccgg 350

cggagaaagg cagctgagcc cggagaagag cgaaatatgg ggacccgggc 400

taaaagcaga cgtcgtcctt cccgcccgct atttctatat tcaggcagtg 450

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caaatcccca tatattttaa aagggccggt ttaccatgag aactgtgact 700

gtcctctgca agatagtgca gcctggctac gggagatgaa ctgccctgaa 750

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aagaagaatt tttttaagta ttaattccat ggacaatata aaatctgtgt 1900

gattgtttgc agtatgaaga cacatttcta cttatgcagt attctcatga 1950

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ttaaaggaaa aaaa 2014

<210> 40
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<212> PRT
<213> Homo Sapien

<400> 40

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Lys Ser Glu Ile Trp Gly Pro Gly Leu Lys Ala Asp Val Val Leu
             35                  40                  45

Pro Ala Arg Tyr Phe Tyr Ile Gln Ala Val Asp Thr Ser Gly Asn
             50                  55                  60

Lys Phe Thr Ser Ser Pro Gly Glu Lys Val Phe Gln Val Lys Val
             65                  70                  75

Ser Ala Pro Glu Glu Gln Phe Thr Arg Val Gly Val Gln Val Leu
             80                  85                  90

Asp Arg Lys Asp Gly Ser Phe Ile Val Arg Tyr Arg Met Tyr Ala
             95                 100                 105

Ser Tyr Lys Asn Leu Lys Val Glu Ile Lys Phe Gln Gly Gln His
            110                 115                 120

Val Ala Lys Ser Pro Tyr Ile Leu Lys Gly Pro Val Tyr His Glu
            125                 130                 135

Asn Cys Asp Cys Pro Leu Gln Asp Ser Ala Ala Trp Leu Arg Glu
            140                 145                 150

Met Asn Cys Pro Glu Thr Ile Ala Gln Ile Gln Arg Asp Leu Ala
            155                 160                 165

His Phe Pro Ala Val Asp Pro Glu Lys Ile Ala Val Glu Ile Pro
            170                 175                 180

Lys Arg Phe Gly Gln Arg Gln Ser Leu Cys His Tyr Thr Leu Lys
            185                 190                 195

Asp Asn Lys Val Tyr Ile Lys Thr His Gly Glu His Val Gly Phe
            200                 205                 210

Arg Ile Phe Met Asp Ala Ile Leu Leu Ser Leu Thr Arg Lys Val
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Lys Met Pro Asp Val Glu Leu Phe Val Asn Leu Gly Asp Trp Pro
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230 235 240

Leu Glu Lys Lys Lys Ser Asn Ser Asn Ile His Pro Ile Phe Ser
245 250 255

Trp Cys Gly Ser Thr Asp Ser Lys Asp Ile Val Met Pro Thr Tyr
260 265 270

Asp Leu Thr Asp Ser Val Leu Glu Thr Met Gly Arg Val Ser Leu
275 280 285

Asp Met Met Ser Val Gln Ala Asn Thr Gly Pro Pro Trp Glu Ser
290 295 300

Lys Asn Ser Thr Ala Val Trp Arg Gly Arg Asp Ser Arg Lys Glu
305 310 315

Arg Leu Glu Leu Val Lys Leu Ser Arg Lys His Pro Glu Leu Ile
320 325 330

Asp Ala Ala Phe Thr Asn Phe Phe Phe Phe Lys His Asp Glu Asn
335 340 345

Leu Tyr Gly Pro Ile Val Lys His Ile Ser Phe Phe Asp Phe Phe
350 355 360

Lys His Lys Tyr Gln Ile Asn Ile Asp Gly Thr Val Ala Ala Tyr
365 370 375

Arg Leu Pro Tyr Leu Leu Val Gly Asp Ser Val Val Leu Lys Gln
380 385 390

Asp Ser Ile Tyr Tyr Glu His Phe Tyr Asn Glu Leu Gln Pro Trp
395 400 405

Lys His Tyr Ile Pro Val Lys Ser Asn Leu Ser Asp Leu Leu Glu
410 415 420

Lys Leu Lys Trp Ala Lys Asp His Asp Glu Glu Ala Lys Lys Ile
425 430 435

Ala Lys Ala Gly Gln Glu Phe Ala Arg Asn Asn Leu Met Gly Asp
440 445 450

Asp Ile Phe Cys Tyr Tyr Phe Lys Leu Phe Gln Glu Tyr Ala Asn
455 460 465

Leu Gln Val Ser Glu Pro Gln Ile Arg Glu Gly Met Lys Arg Val
470 475 480

Glu Pro Gln Thr Glu Asp Asp Leu Phe Pro Cys Thr Cys His Arg
485 490 495

Lys Lys Thr Lys Asp Glu Leu
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<213> Artificial Sequence

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<210> 42
<211> 24
<212> DNA
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<220>
<223> Synthetic oligonucleotide probe

<400> 42
cgataagctg ctacagtgcc atcg 24

<210> 43
<211> 40
<212> DNA
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<220>
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<400> 43
gtgactgtcc tctgcaagat agtgcagcct ggctacggga 40

<210> 44
<211> 2395
<212> DNA
<213> Homo Sapien

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<212> PRT
<213> Homo Sapien

<400> 45

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Pro	Val	Arg	Ser	Ser	Ala	Arg	Ala	Glu	His	Gly	Ala	Glu	Pro	Pro
				35				40						45
Ala	Pro	Glu	Pro	Ser	Ala	Gly	Ala	Ser	Ser	Asn	Trp	Thr	Thr	Leu
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Pro	Pro	Pro	Leu	Phe	Ser	Lys	Val	Val	Ile	Val	Leu	Ile	Asp	Ala
				65				70						75
Leu	Arg	Asp	Asp	Phe	Val	Phe	Gly	Ser	Lys	Gly	Val	Lys	Phe	Met
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Pro	Tyr	Thr	Thr	Tyr	Leu	Val	Glu	Lys	Gly	Ala	Ser	His	Ser	Phe
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Val	Ala	Glu	Ala	Lys	Pro	Pro	Thr	Val	Thr	Met	Pro	Arg	Ile	Lys
				110				115						120
Ala	Leu	Met	Thr	Gly	Ser	Leu	Pro	Gly	Phe	Val	Asp	Val	Ile	Arg
				125				130						135
Asn	Leu	Asn	Ser	Pro	Ala	Leu	Leu	Glu	Asp	Ser	Val	Ile	Arg	Gln
				140				145						150
Ala	Lys	Ala	Ala	Gly	Lys	Arg	Ile	Val	Phe	Tyr	Gly	Asp	Glu	Thr
				155				160						165
Trp	Val	Lys	Leu	Phe	Pro	Lys	His	Phe	Val	Glu	Tyr	Asp	Gly	Thr
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Thr Ser Phe Phe Val Ser Asp Tyr Thr Glu Val Asp Asn Asn Val
185 190 195

Thr Arg His Leu Asp Lys Val Leu Lys Arg Gly Asp Trp Asp Ile
200 205 210

Leu Ile Leu His Tyr Leu Gly Leu Asp His Ile Gly His Ile Ser
215 220 225

Gly Pro Asn Ser Pro Leu Ile Gly Gln Lys Leu Ser Glu Met Asp
230 235 240

Ser Val Leu Met Lys Ile His Thr Ser Leu Gln Ser Lys Glu Arg
245 250 255

Glu Thr Pro Leu Pro Asn Leu Leu Val Leu Cys Gly Asp His Gly
260 265 270

Met Ser Glu Thr Gly Ser His Gly Ala Ser Ser Thr Glu Glu Val
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290 295 300

Gly Asp Ile Arg His Pro Lys His Val Gln
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<212> DNA
<213> Artificial Sequence

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<223> Synthetic oligonucleotide probe

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<210> 47
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 47
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<210> 48
<211> 38
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 48

ccttcgggga ttcttcccgg ctcccgttcg ttcctctg 38

<210> 49
<211> 918
<212> DNA
<213> Homo Sapien

<400> 49
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agccatcgac ctccagggct cctgctgtga ggggtacctc tgcaacagga 700

aatccatgac ccagcccttc accagtgctt cagccaccac ccctccccga 750

gcactacagg tcctggccct gctcctccca gtcctcctgc tggtggggct 800

ctcagcatag accgcccctc caggatgctg gggacagggc tcacacacct 850

cattcttgct gcttcagccc ctatcacata gctcactgga aaatgatgtt 900

aaagtaagaa ttgcaaaa 918

<210> 50
<211> 251
<212> PRT
<213> Homo Sapien

<400> 50
Met Ala Met Gly Val Pro Arg Val Ile Leu Leu Cys Leu Phe Gly
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Ala Ala Leu Cys Leu Thr Gly Ser Gln Ala Leu Gln Cys Tyr Ser
20 25 30

Phe Glu His Thr Tyr Phe Gly Pro Phe Asp Leu Arg Ala Met Lys
35 40 45

Leu Pro Ser Ile Ser Cys Pro His Glu Cys Phe Glu Ala Ile Leu
50 55 60

Ser Leu Asp Thr Gly Tyr Arg Ala Pro Val Thr Leu Val Arg Lys
65 70 75

Gly Cys Trp Thr Gly Pro Pro Ala Gly Gln Thr Gln Ser Asn Pro
80 85 90

Asp Ala Leu Pro Pro Asp Tyr Ser Val Val Arg Gly Cys Thr Thr
95 100 105

Asp Lys Cys Asn Ala His Leu Met Thr His Asp Ala Leu Pro Asn
110 115 120

Leu Ser Gln Ala Pro Asp Pro Pro Thr Leu Ser Gly Ala Glu Cys
125 130 135

Tyr Ala Cys Ile Gly Val His Gln Asp Asp Cys Ala Ile Gly Arg
140 145 150

Ser Arg Arg Val Gln Cys His Gln Asp Gln Thr Ala Cys Phe Gln
155 160 165

Gly Ser Gly Arg Met Thr Val Gly Asn Phe Ser Val Pro Val Tyr
170 175 180

Ile Arg Thr Cys His Arg Pro Ser Cys Thr Thr Glu Gly Thr Thr
185 190 195

Ser Pro Trp Thr Ala Ile Asp Leu Gln Gly Ser Cys Cys Glu Gly
200 205 210

Tyr Leu Cys Asn Arg Lys Ser Met Thr Gln Pro Phe Thr Ser Ala
215 220 225

Ser Ala Thr Thr Pro Pro Arg Ala Leu Gln Val Leu Ala Leu Leu
230 235 240

Leu Pro Val Leu Leu Leu Val Gly Leu Ser Ala
245 250

<210> 51
<211> 3288
<212> DNA
<213> Homo Sapien

<400> 51
cccacgcgtc cgggacagat gaacttaaaa gagaagcttt agctgccaaa 50

gattgggaaa gggaaaggac aaaaaagacc cctgggctac acggcgtagg 100

tgcagggttt cctactgctg ttcttttatg ctgggagctg tggctgtaac 150

caactaggaa ataacgtatg cagcagctat ggctgtcaga gagttgtgct 200

tcccaagaca aaggcaagtc ctgtttcttt ttctttttg gggagtgtcc 250

ttggcaggtt ctgggtttgg acgttattcg gtgactgagg aaacagagaa 300

aggatccttt gtggtcaatc tggcaaagga tctgggacta gcagaggggg 350

agctggctgc aaggggaacc agggtggttt ccgatgataa caaacaatac 400

ctgctcctgg attcacatac cgggaatttg ctcacaaatg agaaactgga 450

ccgagagaag ctgtgtggcc ctaaagagcc ctgtatgctg tatttccaaa 500

ttttaatgga tgatcccttt cagatttacc gggctgagct gagagtcagg 550

gatataaatg atcacgcgcc agtatttcag gacaaagaaa cagtcttaaa 600

aatatcagaa aatacagctg aagggacagc atttagacta gaaagagcac 650

aggatccaga tggaggactt aacggtatcc aaaactacac gatcagcccc 700

aactcttttt tccatattaa cattagtggc ggtgatgaag gcatgatata 750

tccagagcta gtgttggaca aagcactgga tcgggaggag cagggagagc 800

tcagcttaac cctcacagcg ctggatggtg ggtctccatc caggtctggg 850

acctctactg tacgcatcgt tgtcttggac gtcaatgaca atgccccaca 900

gtttgcccag gctctgtatg agacccaggc tccagaaaac agccccattg 950

ggttccttat tgttaaggta tgggcagaag atgtagactc tggagtcaac 1000

gcggaagtat cctattcatt ttttgatgcc tcagaaaata ttcgaacgac 1050

ctttcaaatc aatccttttt ctggggaaat ctttctcaga gaattgcttg 1100

attatgagtt agtaaattct tacaaaataa atatacaggc aatggacggt 1150

ggaggccttt ctgcaagatg tagggtttta gtggaagtat tggacaccaa 1200

tgacaatccc cctgaactga tcgtatcatc attttccaac tctgttgctg 1250

agaattctcc tgagacgccg ctggctgttt ttaagattaa tgacagagac 1300

tctggagaaa atggaaagat ggtttgctac attcaagaga atctgccatt 1350

cctactaaaa ccttctgtgg agaattttta catcctaatt acagaaggcg 1400

cgctggacag agagatcaga gccgagtaca acatcactat caccgtcact 1450

gacttgggga cacccaggct gaaaaccgag cacaacataa cggtcctggt 1500

ctccgacgtc aatgacaacg cccccgcctt cacccaaacc tcctacaccc 1550

tgttcgtccg cgagaacaac agccccgccc tgcacatcgg cagcgtcagc 1600

gccacagaca gagactcggg caccaacgcc caggtcacct actcgctgct 1650

gccgccccaa gacccgcacc tgcccctcgc ctccctggtc tccatcaacg 1700

cggacaacgg ccacctgttc gccctcaggt cgctggacta cgaggccctg 1750

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gagcagagag gcgctggtgc gcgtgctggt gctggacgcc aacgacaact 1850

cgcccttcgt gctgtacccg ctgcagaacg gctccgcgcc ctgcaccgag 1900

ctggtgcccc gggcggccga gccgggctac ctggtgacca aggtggtggc 1950

ggtggacggc gactcgggcc agaacgcctg gctgtcgtac cagctgctca 2000

aggccacgga gcccgggctg ttcggtgtgt gggcgcacaa tggggaggtg 2050

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ggtgcttgtc aaggacaatg gcgagcctcc tcgctcggcc accgccacgc 2150

tgcacttgct cctggtggac ggcttctccc agccctacct gcctctcccg 2200

gaggcggccc cggcccaggc ccaggccgag gccgacttgc tcaccgtcta 2250

cctggtggtg gcgttggcct cggtgtcttc gctcttcctc ctctcggtgc 2300

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gatattcagg cacagggccc tgggaggaag ggtgaagaaa attccacctt 2550

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atctgaggtt ttgattcatt tcagagcttg catctcatga ttctaatcac 2900

ttctgtctat agtgtacttg ctctatttaa gaaggcatat ctacatttcc 2950

aaactcattc taacattcta tatattcgtg tttgaaaacc atgtcattta 3000

tttctacatc atgtatttaa aaagaaatat ttctctacta ctatgctcat 3050

gacaaaatga aacaaagcat attgtgagca atactgaaca tcaataatac 3100

ccttagttta tatacttatt attttatctt taagcatgct acttttactt 3150

ggccaatatt ttcttatgtt aacttttgct gatgtataaa acagactatg 3200

ccttataatt gaaataaaat tataatctgc ctgaaaatga ataaaaataa 3250

aacattttga aatgtgaaaa aaaaaaaaaa aaaaaaa 3288

<210> 52
<211> 800
<212> PRT
<213> Homo Sapien

<400> 52
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1 5 10 15

Phe Leu Phe Leu Phe Trp Gly Val Ser Leu Ala Gly Ser Gly Phe
20 25 30

Gly Arg Tyr Ser Val Thr Glu Glu Thr Glu Lys Gly Ser Phe Val
35 40 45

Val Asn Leu Ala Lys Asp Leu Gly Leu Ala Glu Gly Glu Leu Ala
50 55 60

Ala Arg Gly Thr Arg Val Val Ser Asp Asp Asn Lys Gln Tyr Leu
65 70 75

Leu Leu Asp Ser His Thr Gly Asn Leu Leu Thr Asn Glu Lys Leu
80 85 90

Asp Arg Glu Lys Leu Cys Gly Pro Lys Glu Pro Cys Met Leu Tyr
95 100 105

Phe Gln Ile Leu Met Asp Asp Pro Phe Gln Ile Tyr Arg Ala Glu
110 115 120

Leu Arg Val Arg Asp Ile Asn Asp His Ala Pro Val Phe Gln Asp
125 130 135

Lys Glu Thr Val Leu Lys Ile Ser Glu Asn Thr Ala Glu Gly Thr
140 145 150

Ala Phe Arg Leu Glu Arg Ala Gln Asp Pro Asp Gly Gly Leu Asn
155 160 165

Gly Ile Gln Asn Tyr Thr Ile Ser Pro Asn Ser Phe Phe His Ile
170 175 180

Asn Ile Ser Gly Gly Asp Glu Gly Met Ile Tyr Pro Glu Leu Val
185 190 195

Leu Asp Lys Ala Leu Asp Arg Glu Glu Gln Gly Glu Leu Ser Leu
200 205 210

Thr Leu Thr Ala Leu Asp Gly Gly Ser Pro Ser Arg Ser Gly Thr
215 220 225

Ser Thr Val Arg Ile Val Val Leu Asp Val Asn Asp Asn Ala Pro
230 235 240

Gln Phe Ala Gln Ala Leu Tyr Glu Thr Gln Ala Pro Glu Asn Ser
245 250 255

Pro Ile Gly Phe Leu Ile Val Lys Val Trp Ala Glu Asp Val Asp
260 265 270

Ser Gly Val Asn Ala Glu Val Ser Tyr Ser Phe Phe Asp Ala Ser
275 280 285

Glu Asn Ile Arg Thr Thr Phe Gln Ile Asn Pro Phe Ser Gly Glu
290 295 300

Ile Phe Leu Arg Glu Leu Leu Asp Tyr Glu Leu Val Asn Ser Tyr
305 310 315

Lys Ile Asn Ile Gln Ala Met Asp Gly Gly Gly Leu Ser Ala Arg
320 325 330

Cys Arg Val Leu Val Glu Val Leu Asp Thr Asn Asp Asn Pro Pro
335 340 345

Glu Leu Ile Val Ser Ser Phe Ser Asn Ser Val Ala Glu Asn Ser
350 355 360

Pro Glu Thr Pro Leu Ala Val Phe Lys Ile Asn Asp Arg Asp Ser
365 370 375

Gly Glu Asn Gly Lys Met Val Cys Tyr Ile Gln Glu Asn Leu Pro
380 385 390

Phe Leu Leu Lys Pro Ser Val Glu Asn Phe Tyr Ile Leu Ile Thr
395 400 405

Glu Gly Ala Leu Asp Arg Glu Ile Arg Ala Glu Tyr Asn Ile Thr
410 415 420

Ile Thr Val Thr Asp Leu Gly Thr Pro Arg Leu Lys Thr Glu His
425 430 435

Asn Ile Thr Val Leu Val Ser Asp Val Asn Asp Asn Ala Pro Ala
440 445 450

Phe Thr Gln Thr Ser Tyr Thr Leu Phe Val Arg Glu Asn Asn Ser
455 460 465

Pro Ala Leu His Ile Gly Ser Val Ser Ala Thr Asp Arg Asp Ser
470 475 480

Gly Thr Asn Ala Gln Val Thr Tyr Ser Leu Leu Pro Pro Gln Asp
485 490 495

Pro His Leu Pro Leu Ala Ser Leu Val Ser Ile Asn Ala Asp Asn
500 505 510

Gly His Leu Phe Ala Leu Arg Ser Leu Asp Tyr Glu Ala Leu Gln

515 520 525

Ala Phe Glu Phe Arg Val Gly Ala Thr Asp Arg Gly Ser Pro Ala
530 535 540

Leu Ser Arg Glu Ala Leu Val Arg Val Leu Val Leu Asp Ala Asn
545 550 555

Asp Asn Ser Pro Phe Val Leu Tyr Pro Leu Gln Asn Gly Ser Ala
560 565 570

Pro Cys Thr Glu Leu Val Pro Arg Ala Ala Glu Pro Gly Tyr Leu
575 580 585

Val Thr Lys Val Val Ala Val Asp Gly Asp Ser Gly Gln Asn Ala
590 595 600

Trp Leu Ser Tyr Gln Leu Leu Lys Ala Thr Glu Pro Gly Leu Phe
605 610 615

Gly Val Trp Ala His Asn Gly Glu Val Arg Thr Ala Arg Leu Leu
620 625 630

Ser Glu Arg Asp Ala Ala Lys His Arg Leu Val Val Leu Val Lys
635 640 645

Asp Asn Gly Glu Pro Pro Arg Ser Ala Thr Ala Thr Leu His Leu
650 655 660

Leu Leu Val Asp Gly Phe Ser Gln Pro Tyr Leu Pro Leu Pro Glu
665 670 675

Ala Ala Pro Ala Gln Ala Gln Ala Glu Ala Asp Leu Leu Thr Val
680 685 690

Tyr Leu Val Val Ala Leu Ala Ser Val Ser Ser Leu Phe Leu Leu
695 700 705

Ser Val Leu Leu Phe Val Ala Val Arg Leu Cys Arg Arg Ser Arg
710 715 720

Ala Ala Ser Val Gly Arg Cys Ser Val Pro Glu Gly Pro Phe Pro
725 730 735

Gly His Leu Val Asp Val Arg Gly Ala Glu Thr Leu Ser Gln Ser
740 745 750

Tyr Gln Tyr Glu Val Cys Leu Thr Gly Gly Pro Gly Thr Ser Glu
755 760 765

Phe Lys Phe Leu Lys Pro Val Ile Ser Asp Ile Gln Ala Gln Gly
770 775 780

Pro Gly Arg Lys Gly Glu Glu Asn Ser Thr Phe Arg Asn Ser Phe
785 790 795

Gly Phe Asn Ile Gln
800

<210> 53
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 53
ctggggagtg tccttggcag gttc 24

<210> 54
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 54
cagcatacag ggctctttag ggcacac 27

<210> 55
<211> 46
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 55
cggtgactga ggaaacagag aaaggatcct ttgtggtcaa tctggc 46

<210> 56
<211> 2242
<212> DNA
<213> Homo Sapien

<220>
<221> unsure
<222> 2181
<223> unknown base

<400> 56
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tataccagcc tcgtcttcct tccgggggac aacgtgggtc agggcacaga 100

gagatattta atgtcaccct cttggggctt tcatgggact ccctctgcca 150

catttttgg aggttgggaa agttgctaga ggcttcagaa ctccagccta 200

atggatccca aactcgggag aatggctgcg tccctgctgg ctgtgctgct 250

gctgctgctg gagcgcggca tgttctcctc accctccccg cccccggcgc 300

tgttagagaa agtcttccag tacattgacc tccatcagga tgaatttgtg 350

cagacgctga aggagtgggt ggccatcgag agcgactctg tccagcctgt 400

gcctcgcttc agacaagagc tcttcagaat gatggccgtg gctgcggaca 450

cgctgcagcg cctgggggcc cgtgtggcct cggtggacat gggtcctcag 500

cagctgcccg atggtcagag tcttccaata cctcccgtca tcctggccga 550

actggggagc gatcccacga aaggcaccgt gtgcttctac ggccacttgg 600

acgtgcagcc tgctgaccgg ggcgatgggt ggctcacgga cccctatgtg 650

ctgacggagg tagacgggaa actttatgga cgaggagcga ccgacaacaa 700

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gctggctctg ttgccctgga ggaacttgtg gaaaaagaaa aggaccgatt 850

cttctctggt gtggactaca ttgtaatttc agataacctg tggatcagcc 900

aaaggaagcc agcaatcact tatggaaccc gggggaacag ctacttcatg 950

gtggaggtga aatgcagaga ccaggatttt cactcaggaa cctttggtgg 1000

catccttcat gaaccaatgg ctgatctggt tgctcttctc ggtagcctgg 1050

tagactcgtc tggtcatatc ctggtccctg gaatctatga tgaagtggtt 1100

cctcttacag aagaggaaat aaatacatac aaagccatcc atctagacct 1150

agaagaatac cggaatagca gccgggttga gaaatttctg ttcgatacta 1200

aggaggagat tctaatgcac ctctggaggt acccatctct ttctattcat 1250

gggatcgagg gcgcgtttga tgagcctgga actaaaacag tcatacctgg 1300

ccgagttata ggaaaatttt caatccgtct agtccctcac atgaatgtgt 1350

ctgcggtgga aaaacaggtg acacgacatc ttgaagatgt gttctccaaa 1400

agaaatagtt ccaacaagat ggttgtttcc atgactctag gactacaccc 1450

gtggattgca aatattgatg acacccagta tctcgcagca aaaagagcga 1500

tcagaacagt gtttggaaca gaaccagata tgatccggga tggatccacc 1550

attccaattg ccaaaatgtt ccaggagatc gtccacaaga gcgtggtgct 1600

aattccgctg ggagctgttg atgatggaga acattcgcag aatgagaaaa 1650

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tggattcctt ccaacctttt agcatatctc caaccttgca atttgattgg 2050

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aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aa 2242

<210> 57
<211> 507
<212> PRT
<213> Homo Sapien

<400> 57

Met Asp Pro Lys Leu Gly Arg Met Ala Ala Ser Leu Leu Ala Val
1 5 10 15

Leu Leu Leu Leu Leu Glu Arg Gly Met Phe Ser Ser Pro Ser Pro
20 25 30

Pro Pro Ala Leu Leu Glu Lys Val Phe Gln Tyr Ile Asp Leu His
35 40 45

Gln Asp Glu Phe Val Gln Thr Leu Lys Glu Trp Val Ala Ile Glu
50 55 60

Ser Asp Ser Val Gln Pro Val Pro Arg Phe Arg Gln Glu Leu Phe
65 70 75

Arg Met Met Ala Val Ala Ala Asp Thr Leu Gln Arg Leu Gly Ala
80 85 90

Arg Val Ala Ser Val Asp Met Gly Pro Gln Gln Leu Pro Asp Gly
95 100 105

Gln Ser Leu Pro Ile Pro Pro Val Ile Leu Ala Glu Leu Gly Ser
110 115 120

Asp Pro Thr Lys Gly Thr Val Cys Phe Tyr Gly His Leu Asp Val
125 130 135

Gln Pro Ala Asp Arg Gly Asp Gly Trp Leu Thr Asp Pro Tyr Val
140 145 150

Leu Thr Glu Val Asp Gly Lys Leu Tyr Gly Arg Gly Ala Thr Asp
155 160 165

Asn Lys Gly Pro Val Leu Ala Trp Ile Asn Ala Val Ser Ala Phe

170 175 180

Arg Ala Leu Glu Gln Asp Leu Pro Val Asn Ile Lys Phe Ile Ile
185 190 195

Glu Gly Met Glu Glu Ala Gly Ser Val Ala Leu Glu Glu Leu Val
200 205 210

Glu Lys Glu Lys Asp Arg Phe Phe Ser Gly Val Asp Tyr Ile Val
215 220 225

Ile Ser Asp Asn Leu Trp Ile Ser Gln Arg Lys Pro Ala Ile Thr
230 235 240

Tyr Gly Thr Arg Gly Asn Ser Tyr Phe Met Val Glu Val Lys Cys
245 250 255

Arg Asp Gln Asp Phe His Ser Gly Thr Phe Gly Gly Ile Leu His
260 265 270

Glu Pro Met Ala Asp Leu Val Ala Leu Leu Gly Ser Leu Val Asp
275 280 285

Ser Ser Gly His Ile Leu Val Pro Gly Ile Tyr Asp Glu Val Val
290 295 300

Pro Leu Thr Glu Glu Glu Ile Asn Thr Tyr Lys Ala Ile His Leu
305 310 315

Asp Leu Glu Glu Tyr Arg Asn Ser Ser Arg Val Glu Lys Phe Leu
320 325 330

Phe Asp Thr Lys Glu Glu Ile Leu Met His Leu Trp Arg Tyr Pro
335 340 345

Ser Leu Ser Ile His Gly Ile Glu Gly Ala Phe Asp Glu Pro Gly
350 355 360

Thr Lys Thr Val Ile Pro Gly Arg Val Ile Gly Lys Phe Ser Ile
365 370 375

Arg Leu Val Pro His Met Asn Val Ser Ala Val Glu Lys Gln Val
380 385 390

Thr Arg His Leu Glu Asp Val Phe Ser Lys Arg Asn Ser Ser Asn
395 400 405

Lys Met Val Val Ser Met Thr Leu Gly Leu His Pro Trp Ile Ala
410 415 420

Asn Ile Asp Asp Thr Gln Tyr Leu Ala Ala Lys Arg Ala Ile Arg
425 430 435

Thr Val Phe Gly Thr Glu Pro Asp Met Ile Arg Asp Gly Ser Thr
440 445 450

Ile Pro Ile Ala Lys Met Phe Gln Glu Ile Val His Lys Ser Val
455 460 465

Val Leu Ile Pro Leu Gly Ala Val Asp Asp Gly Glu His Ser Gln
470 475 480

Asn Glu Lys Ile Asn Arg Trp Asn Tyr Ile Glu Gly Thr Lys Leu
485 490 495

Phe Ala Ala Phe Phe Leu Glu Met Ala Gln Leu His
500 505

<210> 58
<211> 1470
<212> DNA
<213> Homo Sapien

<400> 58
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acactacctt cccgaagttg aaggcaagcg gtgattgttt gtagacggcg 100

ctttgtcatg ggacctgtgc ggttgggaat attgcttttc ctttttttgg 150

ccgtgcacga ggcttgggct gggatgttga aggaggagga cgatgacaca 200

gaacgcttgc ccagcaaatg cgaagtgtgt aagctgctga gcacagagct 250

acaggcggaa ctgagtcgca ccggtcgatc tcgagaggtg ctggagctgg 300

ggcaggtgct ggatacaggc aagaggaaga gacacgtgcc ttacagcgtt 350

tcagagacaa ggctggaaga ggccttagag aatttatgtg agcggatcct 400

ggactatagt gttcacgctg agcgcaaggg ctcactgaga tatgccaagg 450

gtcagagtca gaccatggca acactgaaag gcctagtgca gaaggggtg 500

aaggtggatc tggggatccc tctggagctt tgggatgagc ccagcgtgga 550

ggtcacatac ctcaagaagc agtgtgagac catgttggag gagtttgaag 600

acattgtggg agactggtac ttccaccatc aggagcagcc cctacaaaat 650

tttctctgtg aaggtcatgt gctcccagct gctgaaactg catgtctaca 700

ggaaacttgg actggaaagg agatcacaga tggggaagag aaaacagaag 750

gggaggaaga gcaggaggag gaggaggaag aggaggaaga ggaaggggga 800

gacaagatga ccaagacagg aagccacccc aaacttgacc gagaagatct 850

ttgacccttg cctttgagcc cccaggaggg gaagggatca tggagagccc 900

tctaaagcct gcactctccc tgctccacag ctttcagggt gtgtttatga 950

gtgactccac ccaagcttgt agctgttctc tcccatctaa cctcaggcaa 1000

gatcctggtg aaacagcatg acatggcttc tggggtggag ggtgggggtg 1050

gaggtcctgc tcctagagat gaactctatc cagcccctta attggcaggt 1100

gtatgtgctg acagtactga aagctttcct ctttaactga tcccaccccc 1150

acccaaaagt cagcagtggc actggagctg tgggctttgg ggaagtcact 1200

tagctcctta aggtctgttt ttagaccctt ccaaggaaga ggccagaacg 1250

gacattctct gcgatctata tacattgcct gtatccagga ggctacacac 1300

cagcaaaccg tgaaggagaa tgggacactg ggtcatggcc tggagttgct 1350

gataatttag gtgggataga tacttggtct acttaagctc aatgtaaccc 1400

agagcccacc atatagtttt ataggtgctc aactttctat atcgctatta 1450

aacttttttc ttttttttcta 1470

<210> 59
<211> 248
<212> PRT
<213> Homo Sapien

<400> 59

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Val	His	Glu	Ala	Trp	Ala	Gly	Met	Leu	Lys	Glu	Glu	Asp	Asp	Asp
				20				25						30
Thr	Glu	Arg	Leu	Pro	Ser	Lys	Cys	Glu	Val	Cys	Lys	Leu	Leu	Ser
				35				40						45
Thr	Glu	Leu	Gln	Ala	Glu	Leu	Ser	Arg	Thr	Gly	Arg	Ser	Arg	Glu
				50				55						60
Val	Leu	Glu	Leu	Gly	Gln	Val	Leu	Asp	Thr	Gly	Lys	Arg	Lys	Arg
				65				70						75
His	Val	Pro	Tyr	Ser	Val	Ser	Glu	Thr	Arg	Leu	Glu	Glu	Ala	Leu
				80				85						90
Glu	Asn	Leu	Cys	Glu	Arg	Ile	Leu	Asp	Tyr	Ser	Val	His	Ala	Glu
				95				100						105
Arg	Lys	Gly	Ser	Leu	Arg	Tyr	Ala	Lys	Gly	Gln	Ser	Gln	Thr	Met
				110				115						120
Ala	Thr	Leu	Lys	Gly	Leu	Val	Gln	Lys	Gly	Val	Lys	Val	Asp	Leu
				125				130						135
Gly	Ile	Pro	Leu	Glu	Leu	Trp	Asp	Glu	Pro	Ser	Val	Glu	Val	Thr
				140				145						150
Tyr	Leu	Lys	Lys	Gln	Cys	Glu	Thr	Met	Leu	Glu	Glu	Phe	Glu	Asp
				155				160						165
Ile	Val	Gly	Asp	Trp	Tyr	Phe	His	His	Gln	Glu	Gln	Pro	Leu	Gln
				170				175						180

Asn Phe Leu Cys Glu Gly His Val Leu Pro Ala Ala Glu Thr Ala
185 190 195

Cys Leu Gln Glu Thr Trp Thr Gly Lys Glu Ile Thr Asp Gly Glu
200 205 210

Glu Lys Thr Glu Gly Glu Glu Glu Gln Glu Glu Glu Glu Glu Glu
215 220 225

Glu Glu Glu Glu Gly Gly Asp Lys Met Thr Lys Thr Gly Ser His
230 235 240

Pro Lys Leu Asp Arg Glu Asp Leu
245

<210> 60
<211> 890
<212> DNA
<213> Homo Sapien

<400> 60
aagtacttgt gtccgggtgg tggactggat tagctgcgga gccctggaag 50

ctgcctgtcc ttctccctgt gcttaaccag aggtgcccat gggttggaca 100

atgaggctgg tcacagcagc actgttactg ggtctcatga tggtggtcac 150

tggagacgag gatgagaaca gcccgtgtgc ccatgaggcc ctcttggacg 200

aggacaccct cttttgccag ggccttgaag ttttctaccc agagttgggg 250

aacattggct gcaaggttgt tcctgattgt aacaactaca gacagaagat 300

cacctcctgg atggagccga tagtcaagtt cccgggggcc gtggacggcg 350

caacctatat cctggtgatg gtggatccag atgcccctag cagagcagaa 400

cccagacaga gattctggag acattggctg gtaacagata tcaagggcgc 450

cgacctgaag aaagggaaga ttcagggcca ggagttatca gcctaccagg 500

ctccctcccc accggcacac agtggcttcc atcgctacca gttctttgtc 550

tatcttcagg aaggaaaagt catctctctc cttcccaagg aaaacaaaac 600

tcgaggctct tggaaaatgg acagatttct gaaccgcttc cacctgggcg 650

aacctgaagc aagcacccag ttcatgaccc agaactacca ggactcacca 700

accctccagg ctcccagagg aagggccagc gagcccaagc acaaaaccag 750

gcagagatag ctgcctgcta gatagccggc tttgccatcc gggcatgtgg 800

ccacactgct caccaccgac gatgtgggta tggaaccccc tctggataca 850

gaaccccttc ttttccaaat taaaaaaaaa aatcatcaaa 890

<210> 61

<211> 223
<212> PRT
<213> Homo Sapien

<400> 61
Met Gly Trp Thr Met Arg Leu Val Thr Ala Ala Leu Leu Leu Gly
1 5 10 15

Leu Met Met Val Val Thr Gly Asp Glu Asp Glu Asn Ser Pro Cys
20 25 30

Ala His Glu Ala Leu Leu Asp Glu Asp Thr Leu Phe Cys Gln Gly
35 40 45

Leu Glu Val Phe Tyr Pro Glu Leu Gly Asn Ile Gly Cys Lys Val
50 55 60

Val Pro Asp Cys Asn Asn Tyr Arg Gln Lys Ile Thr Ser Trp Met
65 70 75

Glu Pro Ile Val Lys Phe Pro Gly Ala Val Asp Gly Ala Thr Tyr
80 85 90

Ile Leu Val Met Val Asp Pro Asp Ala Pro Ser Arg Ala Glu Pro
95 100 105

Arg Gln Arg Phe Trp Arg His Trp Leu Val Thr Asp Ile Lys Gly
110 115 120

Ala Asp Leu Lys Lys Gly Lys Ile Gln Gly Gln Glu Leu Ser Ala
125 130 135

Tyr Gln Ala Pro Ser Pro Pro Ala His Ser Gly Phe His Arg Tyr
140 145 150

Gln Phe Phe Val Tyr Leu Gln Glu Gly Lys Val Ile Ser Leu Leu
155 160 165

Pro Lys Glu Asn Lys Thr Arg Gly Ser Trp Lys Met Asp Arg Phe
170 175 180

Leu Asn Arg Phe His Leu Gly Glu Pro Glu Ala Ser Thr Gln Phe
185 190 195

Met Thr Gln Asn Tyr Gln Asp Ser Pro Thr Leu Gln Ala Pro Arg
200 205 210

Gly Arg Ala Ser Glu Pro Lys His Lys Thr Arg Gln Arg
215 220

<210> 62
<211> 1321
<212> DNA
<213> Homo Sapien

<400> 62
gtcgacccac gcgtccgaag ctgctggagc cacgattcag tcccctggac 50

tgtagataaa gacccttttct tgccaggtgc tgagacaacc acactatgag 100

aggcactcca ggagacgctg atggtggagg aagggccgtc tatcaatcaa 150

tcactgttgc tgttatcaca tgcaagtatc cagaggctct tgagcaaggc 200

agaggggatc ccatttattt gggaatccag aatccagaaa tgtgtttgta 250

ttgtgagaag gttggagaac agcccacatt gcagctaaaa gagcagaaga 300

tcatggatct gtatggccaa cccgagcccg tgaaaccctt ccttttctac 350

cgtgccaaga ctggtaggac ctccaccctt gagtctgtgg ccttcccgga 400

ctggttcatt gcctcctcca agagagacca gcccatcatt ctgacttcag 450

aacttgggaa gtcatacaac actgcctttg aattaaatat aaatgactga 500

actcagccta gaggtggcag cttggtcttt gtcttaaagt ttctggttcc 550

caatgtgttt tcgtctacat tttcttagtg tcattttcac gctggtgctg 600

agacaggagc aaggctgctg ttatcatctc attttataat gaagaagaag 650

caattacttc atagcaactg aagaacagga tgtggcctca gaagcaggag 700

agctgggtgg tataaggctg tcctctcaag ctggtgctgt gtaggccaca 750

aggcatctgc atgagtgact ttaagactca aagaccaaac actgagcttt 800

cttctagggg tgggtatgaa gatgcttcag agctcatgcg cgttacccac 850

gatggcatga ctagcacaga gctgatctct gtttctgttt tgctttattc 900

cctcttggga tgatatcatc cagtctttat atgttgccaa tatacctcat 950

tgtgtgtaat agaaccttct tagcattaag accttgtaaa caaaaataat 1000

tcttggggtg ggtatgaaga tgcttcagag ctcatgcgcg ttacccacga 1050

tggcatgact agcacagagc tgatctctgt ttctgttttg ctttattccc 1100

tcttgggatg atatcatcca gtctttatat gttgccaata tacctcattg 1150

tgtgtaatag aaccttctta gcattaagac cttgtaaaca aaaataattc 1200

ttgtgttaag ttaaatcatt tttgtcctaa ttgtaatgtg taatcttaaa 1250

gttaaataaa ctttgtgtat ttatataata ataaagctaa aactgatata 1300

aaataaagaa agagtaaact g 1321

<210> 63
<211> 134
<212> PRT
<213> Homo Sapien

<400> 63

Met Arg Gly Thr Pro Gly Asp Ala Asp Gly Gly Gly Arg Ala Val
1 5 10 15

Tyr Gln Ser Ile Thr Val Ala Val Ile Thr Cys Lys Tyr Pro Glu
20 25 30

Ala Leu Glu Gln Gly Arg Gly Asp Pro Ile Tyr Leu Gly Ile Gln
35 40 45

Asn Pro Glu Met Cys Leu Tyr Cys Glu Lys Val Gly Glu Gln Pro
50 55 60

Thr Leu Gln Leu Lys Glu Gln Lys Ile Met Asp Leu Tyr Gly Gln
65 70 75

Pro Glu Pro Val Lys Pro Phe Leu Phe Tyr Arg Ala Lys Thr Gly
80 85 90

Arg Thr Ser Thr Leu Glu Ser Val Ala Phe Pro Asp Trp Phe Ile
95 100 105

Ala Ser Ser Lys Arg Asp Gln Pro Ile Ile Leu Thr Ser Glu Leu
110 115 120

Gly Lys Ser Tyr Asn Thr Ala Phe Glu Leu Asn Ile Asn Asp
125 130

<210> 64
<211> 999
<212> DNA
<213> Homo Sapien

<400> 64
gcgaggctgc accagcgcct ggcaccatga ggacgcctgg gcctctgccc 50

gtgctgctgc tgctcctggc gggagccccc gccgcgcggc ccactccccc 100

gacctgctac tcccgcatgc gggccctgag ccaggagatc acccgcgact 150

tcaacctcct gcaggtctcg gagccctcgg agccatgtgt gagatacctg 200

cccaggctgt acctggacat acacaattac tgtgtgctgg acaagctgcg 250

ggactttgtg gcctcgcccc cgtgttggaa agtggcccag gtagattcct 300

tgaaggacaa agcacggaag ctgtacacca tcatgaactc gttctgcagg 350

agagatttgg tattcctgtt ggatgactgc aatgccttgg aatacccaat 400

cccagtgact acggtcctgc cagatcgtca gcgctaaggg aactgagacc 450

agagaaagaa cccaagagaa ctaaagttat gtcagctacc cagacttaat 500

gggccagagc catgaccctc acaggtcttg tgttagttgt atctgaaact 550

gttatgtatc tctctacctt ctggaaaaca gggctggtat tcctacccag 600

gaacctcctt tgagcataga gttagcaacc atgcttctca ttcccttgac 650

tcatgtcttg ccaggatggt tagatacaca gcatgttgat ttggtcacta 700

aaaagaagaa aaggactaac aagcttcact tttatgaaca actattttga 750

gaacatgcac aatagtatgt ttttattact ggtttaatgg agtaatggta 800

cttttattct ttcttgatag aaacctgctt acatttaacc aagcttctat 850

tatgcctttt tctaacacag actttcttca ctgtctttca tttaaaaaga 900

aattaatgct cttaagatat atattttacg tagtgctgac aggacccact 950

ctttcattga aaggtgatga aaatcaaata aagaatctct tcacatgga 999

<210> 65
<211> 136
<212> PRT
<213> Homo Sapien

<400> 65

Met	Arg	Thr	Pro	Gly	Pro	Leu	Pro	Val	Leu	Leu	Leu	Leu	Leu	Ala	
1				5				10						15	
Gly	Ala	Pro	Ala	Ala	Arg	Pro	Thr	Pro	Pro	Thr	Cys	Tyr	Ser	Arg	
				20				25						30	
Met	Arg	Ala	Leu	Ser	Gln	Glu	Ile	Thr	Arg	Asp	Phe	Asn	Leu	Leu	
				35				40						45	
Gln	Val	Ser	Glu	Pro	Ser	Glu	Pro	Cys	Val	Arg	Tyr	Leu	Pro	Arg	
				50				55						60	
Leu	Tyr	Leu	Asp	Ile	His	Asn	Tyr	Cys	Val	Leu	Asp	Lys	Leu	Arg	
				65				70						75	
Asp	Phe	Val	Ala	Ser	Pro	Pro	Cys	Trp	Lys	Val	Ala	Gln	Val	Asp	
				80				85						90	
Ser	Leu	Lys	Asp	Lys	Ala	Arg	Lys	Leu	Tyr	Thr	Ile	Met	Asn	Ser	
				95				100						105	
Phe	Cys	Arg	Arg	Asp	Leu	Val	Phe	Leu	Leu	Asp	Asp	Cys	Asn	Ala	
				110				115						120	
Leu	Glu	Tyr	Pro	Ile	Pro	Val	Thr	Thr	Val	Leu	Pro	Asp	Arg	Gln	
				125				130						135	

Arg

<210> 66
<211> 1893
<212> DNA
<213> Homo Sapien

<400> 66
gtctccgcgt cacaggaact tcagcaccca cagggcggac agcgctcccc 50

tctacctgga gacttgactc ccgcgcgccc caaccctgct tatcccttga 100

ccgtcgagtg tcagagatcc tgcagccgcc cagtcccggc ccctctcccg 150

ccccacaccc accctcctgg ctcttcctgt ttttactcct ccttttcatt 200

cataacaaaa gctacagctc caggagccca gcgccgggct gtgacccaag 250

ccgagcgtgg aagaatgggg ttcctcggga ccggcacttg gattctggtg 300

ttagtgctcc cgattcaagc tttccccaaa cctggaggaa gccaagacaa 350

atctctacat aatagagaat taagtgcaga aagacctttg aatgaacaga 400

ttgctgaagc agaagaagac aagattaaaa aaacatatcc tccagaaaac 450

aagccaggtc agagcaacta ttcttttgtt gataacttga acctgctaaa 500

ggcaataaca gaaaaggaaa aaattgagaa agaaagacaa tctataagaa 550

gctccccact tgataataag ttgaatgtgg aagatgttga ttcaaccaag 600

aatcgaaaac tgatcgatga ttatgactct actaagagtg gattggatca 650

taaatttcaa gatgatccag atggtcttca tcaactagac gggactcctt 700

taaccgctga agacattgtc cataaaatcg ctgccaggat ttatgaagaa 750

aatgacagag ccgtgtttga caagattgtt tctaaactac ttaatctcgg 800

ccttatcaca gaaagccaag cacatacact ggaagatgaa gtagcagagg 850

ttttacaaaa attaatctca aaggaagcca acaattatga ggaggatccc 900

aataagccca caagctggac tgagaatcag gctggaaaaa taccagagaa 950

agtgactcca atggcagcaa ttcaagatgg tcttgctaag ggagaaaacg 1000

atgaaacagt atctaacaca ttaaccttga caaatggctt ggaaaggaga 1050

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tttctatgcg ctactgaaaa gtattgattc agaaaaagaa gcaaaagaga 1150

aagaaacact gattactatc atgaaaacac tgattgactt tgtgaagatg 1200

atggtgaaat atggaacaat atctccagaa gaaggtgttt cctaccttga 1250

aaacttggat gaaatgattg ctcttcagac caaaaacaag ctagaaaaaa 1300

atgctactga caatataagc aagcttttcc cagcaccatc agagaagagt 1350

catgaagaaa cagacagtac caaggaagaa gcagctaaga tggaaaagga 1400

atatggaagc ttgaaggatt ccacaaaaga tgataactcc aacccaggag 1450

gaaagacaga tgaacccaaa ggaaaaacag aagcctattt ggaagccatc 1500

agaaaaaata ttgaatggtt gaagaaacat gacaaaaagg gaaataaaga 1550

agattatgac ctttcaaaga tgagagactt catcaataaa caagctgatg 1600

cttatgtgga gaaaggcatc cttgacaagg aagaagccga ggccatcaag 1650

cgcatttata gcagcctgta aaaatggcaa aagatccagg agtctttcaa 1700

ctgtttcaga aaacataata tagcttaaaa cacttctaat tctgtgatta 1750

aaatttttg acccaagggt tattagaaag tgctgaattt acagtagtta 1800

acctttttaca agtggttaaa acatagcttt cttcccgtaa aaactatctg 1850

aaagtaaagt tgtatgtaag ctgaaaaaaa aaaaaaaaaa aaa 1893

<210> 67
<211> 468
<212> PRT
<213> Homo Sapien

<400> 67

Met	Gly	Phe	Leu	Gly	Thr	Gly	Thr	Trp	Ile	Leu	Val	Leu	Val	Leu	
1				5					10						15
Pro	Ile	Gln	Ala	Phe	Pro	Lys	Pro	Gly	Gly	Ser	Gln	Asp	Lys	Ser	
				20					25						30
Leu	His	Asn	Arg	Glu	Leu	Ser	Ala	Glu	Arg	Pro	Leu	Asn	Glu	Gln	
				35					40						45
Ile	Ala	Glu	Ala	Glu	Glu	Asp	Lys	Ile	Lys	Lys	Thr	Tyr	Pro	Pro	
				50					55						60
Glu	Asn	Lys	Pro	Gly	Gln	Ser	Asn	Tyr	Ser	Phe	Val	Asp	Asn	Leu	
				65					70						75
Asn	Leu	Leu	Lys	Ala	Ile	Thr	Glu	Lys	Glu	Lys	Ile	Glu	Lys	Glu	
				80					85						90
Arg	Gln	Ser	Ile	Arg	Ser	Ser	Pro	Leu	Asp	Asn	Lys	Leu	Asn	Val	
				95					100						105
Glu	Asp	Val	Asp	Ser	Thr	Lys	Asn	Arg	Lys	Leu	Ile	Asp	Asp	Tyr	
				110					115						120
Asp	Ser	Thr	Lys	Ser	Gly	Leu	Asp	His	Lys	Phe	Gln	Asp	Asp	Pro	
				125					130						135
Asp	Gly	Leu	His	Gln	Leu	Asp	Gly	Thr	Pro	Leu	Thr	Ala	Glu	Asp	
				140					145						150
Ile	Val	His	Lys	Ile	Ala	Ala	Arg	Ile	Tyr	Glu	Glu	Asn	Asp	Arg	
				155					160						165
Ala	Val	Phe	Asp	Lys	Ile	Val	Ser	Lys	Leu	Leu	Asn	Leu	Gly	Leu	
				170					175						180

Ile Thr Glu Ser Gln Ala His Thr Leu Glu Asp Glu Val Ala Glu
185 190 195

Val Leu Gln Lys Leu Ile Ser Lys Glu Ala Asn Asn Tyr Glu Glu
200 205 210

Asp Pro Asn Lys Pro Thr Ser Trp Thr Glu Asn Gln Ala Gly Lys
215 220 225

Ile Pro Glu Lys Val Thr Pro Met Ala Ala Ile Gln Asp Gly Leu
230 235 240

Ala Lys Gly Glu Asn Asp Glu Thr Val Ser Asn Thr Leu Thr Leu
245 250 255

Thr Asn Gly Leu Glu Arg Arg Thr Lys Thr Tyr Ser Glu Asp Asn
260 265 270

Phe Glu Glu Leu Gln Tyr Phe Pro Asn Phe Tyr Ala Leu Leu Lys
275 280 285

Ser Ile Asp Ser Glu Lys Glu Ala Lys Glu Lys Glu Thr Leu Ile
290 295 300

Thr Ile Met Lys Thr Leu Ile Asp Phe Val Lys Met Met Val Lys
305 310 315

Tyr Gly Thr Ile Ser Pro Glu Glu Gly Val Ser Tyr Leu Glu Asn
320 325 330

Leu Asp Glu Met Ile Ala Leu Gln Thr Lys Asn Lys Leu Glu Lys
335 340 345

Asn Ala Thr Asp Asn Ile Ser Lys Leu Phe Pro Ala Pro Ser Glu
350 355 360

Lys Ser His Glu Glu Thr Asp Ser Thr Lys Glu Glu Ala Ala Lys
365 370 375

Met Glu Lys Glu Tyr Gly Ser Leu Lys Asp Ser Thr Lys Asp Asp
380 385 390

Asn Ser Asn Pro Gly Gly Lys Thr Asp Glu Pro Lys Gly Lys Thr
395 400 405

Glu Ala Tyr Leu Glu Ala Ile Arg Lys Asn Ile Glu Trp Leu Lys
410 415 420

Lys His Asp Lys Lys Gly Asn Lys Glu Asp Tyr Asp Leu Ser Lys
425 430 435

Met Arg Asp Phe Ile Asn Lys Gln Ala Asp Ala Tyr Val Glu Lys
440 445 450

Gly Ile Leu Asp Lys Glu Glu Ala Glu Ala Ile Lys Arg Ile Tyr
455 460 465

Ser Ser Leu

<210> 68
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 68
cgtcacagga acttcagcac cc 22

<210> 69
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 69
gtcttggctt cctccaggtt tgg 23

<210> 70
<211> 38
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 70
ggacagcgct cccctctacc tggagacttg actcccgc 38

<210> 71
<211> 2379
<212> DNA
<213> Homo Sapien

<400> 71
gttgctccgg cggcgctcgg ggagggagcc agcagcctag ggcctaggcc 50

cgggccacca tggcgctgcc tccaggccca gccgccctcc ggcacacact 100

gctgctcctg ccagcccttc tgagctcagg ttgggggggag ttggagccac 150

aaatagatgg tcagacctgg gctgagcggg cacttcggga gaatgaacgc 200

cacgccttca cctgccgggt ggcaggggggg cctggcaccc ccagattggc 250

ctggtatctg gatggacagc tgcaggaggc cagcacctca agactgctga 300

gcgtgggagg ggaggccttc tctggaggca ccagcacctt cactgtcact 350

gcccatcggg cccagcatga gctcaactgc tctctgcagg accccagaag 400

tggccgatca gccaacgcct ctgtcatcct taatgtgcaa ttcaagccag 450

agattgccca agtcggcgcc aagtaccagg aagctcaggg cccaggcctc 500

ctggttgtcc tgtttgccct ggtgcgtgcc aacccgccgg ccaatgtcac 550

ctggatcgac caggatgggc cagtgactgt caacacctct gacttcctgg 600

tgctggatgc gcagaactac ccctggctca ccaaccacac ggtgcagctg 650

cagctccgca gcctggcaca caacctctcg gtggtggcca ccaatgacgt 700

gggtgtcacc agtgcgtcgc ttccagcccc aggcccctcc cggcacccat 750

ctctgatatc aagtgactcc aacaacctaa aactcaacaa cgtgcgcctg 800

ccacgggaga acatgtccct cccgtccaac cttcagctca atgacctcac 850

tccagattcc agagcagtga aaccagcaga ccggcagatg gctcagaaca 900

acagccggcc agagcttctg gacccggagc ccggcggcct cctcaccagc 950

caaggtttca tccgcctccc agtgctgggc tatatctatc gagtgtccag 1000

cgtgagcagt gatgagatct ggctctgagc cgagggcgag acaggagtat 1050

tctcttggcc tctggacacc ctcccattcc tccaaggcat cctctaccta 1100

gctaggtcac caacgtgaag aagttatgcc actgccactt ttgcttgccc 1150

tcctggctgg ggtgccctcc atgtcatgca cgtgatgcat ttcactgggc 1200

tgtaacccgc aggggcacag gtatctttgg caaggctacc agttggacgt 1250

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aagtgtggca tggcctgctg tataccccac cccagtactc cacagcacct 1400

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catggatttt cctccttcct atgctatgta gccttgttcc ctcaggtaaa 1500

atttaggacc ctgctagctg tgcagaaccc aattgccctt tgcacagaaa 1550

ccaacccctg acccagcggt accggccaag cacaaacgtc ctttttgctg 1600

cacacgtctc tgcccttcac ttcttctctt ctgtccccac ctcctcttgg 1650

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tctgggattc actgtgagtg tcctgagctc tcggggttga tggtttttct 1950

ctcagcatgt ctcctccacc acgggacccc agccctgacc aacccatggt 2000

tgcctcatca gcaggaaggt gcccttcctg gaggatggtc gccacaggca 2050

cataattcaa cagtgtggaa gctttagggg aacatggaga aagaaggaga 2100

ccacataccc caaagtgacc taagaacact ttaaaaagca acatgtaaat 2150

gattggaaat taatatagta cagaatatat ttttcccttg ttgagatctt 2200

cttttgtaat gtttttcatg ttactgccta gggcggtgct gagcacacag 2250

caagtttaat aaacttgact gaattcattt aaaaaaaaaa aaaaaaaaaa 2300

aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 2350

aaaaaaaaaa aaaaaaaaaa aaaaaaaaa 2379

<210> 72
<211> 322
<212> PRT
<213> Homo Sapien

<400> 72

Met Ala Leu Pro Pro Gly Pro Ala Ala Leu Arg His Thr Leu Leu
1 5 10 15

Leu Leu Pro Ala Leu Leu Ser Ser Gly Trp Gly Glu Leu Glu Pro
20 25 30

Gln Ile Asp Gly Gln Thr Trp Ala Glu Arg Ala Leu Arg Glu Asn
35 40 45

Glu Arg His Ala Phe Thr Cys Arg Val Ala Gly Gly Pro Gly Thr
50 55 60

Pro Arg Leu Ala Trp Tyr Leu Asp Gly Gln Leu Gln Glu Ala Ser
65 70 75

Thr Ser Arg Leu Leu Ser Val Gly Gly Glu Ala Phe Ser Gly Gly
80 85 90

Thr Ser Thr Phe Thr Val Thr Ala His Arg Ala Gln His Glu Leu
95 100 105

Asn Cys Ser Leu Gln Asp Pro Arg Ser Gly Arg Ser Ala Asn Ala
110 115 120

Ser Val Ile Leu Asn Val Gln Phe Lys Pro Glu Ile Ala Gln Val
125 130 135

Gly Ala Lys Tyr Gln Glu Ala Gln Gly Pro Gly Leu Leu Val Val
140 145 150

Leu Phe Ala Leu Val Arg Ala Asn Pro Pro Ala Asn Val Thr Trp
155 160 165

Ile Asp Gln Asp Gly Pro Val Thr Val Asn Thr Ser Asp Phe Leu
170 175 180

Val Leu Asp Ala Gln Asn Tyr Pro Trp Leu Thr Asn His Thr Val
185 190 195

Gln Leu Gln Leu Arg Ser Leu Ala His Asn Leu Ser Val Val Ala
200 205 210

Thr Asn Asp Val Gly Val Thr Ser Ala Ser Leu Pro Ala Pro Gly
215 220 225

Pro Ser Arg His Pro Ser Leu Ile Ser Ser Asp Ser Asn Asn Leu
230 235 240

Lys Leu Asn Asn Val Arg Leu Pro Arg Glu Asn Met Ser Leu Pro
245 250 255

Ser Asn Leu Gln Leu Asn Asp Leu Thr Pro Asp Ser Arg Ala Val
260 265 270

Lys Pro Ala Asp Arg Gln Met Ala Gln Asn Asn Ser Arg Pro Glu
275 280 285

Leu Leu Asp Pro Glu Pro Gly Gly Leu Leu Thr Ser Gln Gly Phe
290 295 300

Ile Arg Leu Pro Val Leu Gly Tyr Ile Tyr Arg Val Ser Ser Val
305 310 315

Ser Ser Asp Glu Ile Trp Leu
320

<210> 73
<211> 843
<212> DNA
<213> Homo Sapien

<400> 73
cggggacgga agcggcccct gggcccgagg ggctggagcc gggccggggc 50

gatgtggagc gcgggccgcg gcggggctgc ctggccggtg ctgttggggc 100

tgctgctggc gctgttagtg ccgggcggtg gtgccgccaa gaccggtgcg 150

gagctcgtga cctgcgggtc ggtgctgaag ctgctcaata cgcaccaccg 200

cgtgcggctg cactcgcacg acatcaaata cggatccggc agcggccagc 250

aatcggtgac cggcgtagag gcgtcggacg acgccaatag ctactggcgg 300

atccgcggcg gctcggaggg cgggtgcccg cgcgggtccc cggtgcgctg 350

cgggcaggcg gtgaggctca cgcatgtgct tacgggcaag aacctgcaca 400

cgcaccactt cccgtcgccg ctgtccaaca accaggaggt gagtgccttt 450

ggggaagacg gcgagggcga cgacctggac ctatggacag tgcgctgctc 500

tggacagcac tgggagcgtg aggctgctgt gcgcttccag catgtgggca 550

cctctgtgtt cctgtcagtc acgggtgagc agtatggaag ccccatccgt 600

gggcagcatg aggtccacgg catgcccagt gccaacacgc acaatacgtg 650

gaaggccatg gaaggcatct tcatcaagcc tagtgtggag ccctctgcag 700

gtcacgatga actctgagtg tgtggatgga tgggtggatg gagggtggca 750

ggtggggcgt ctgcagggcc actcttggca gagactttgg gtttgtaggg 800

gtcctcaagt gcctttgtga ttaaagaatg ttggtctatg aaa 843

<210> 74
<211> 221
<212> PRT
<213> Homo Sapien

<400> 74

Met Trp Ser Ala Gly Arg Gly Gly Ala Ala Trp Pro Val Leu Leu
1 5 10 15

Gly Leu Leu Leu Ala Leu Leu Val Pro Gly Gly Gly Ala Ala Lys
20 25 30

Thr Gly Ala Glu Leu Val Thr Cys Gly Ser Val Leu Lys Leu Leu
35 40 45

Asn Thr His His Arg Val Arg Leu His Ser His Asp Ile Lys Tyr
50 55 60

Gly Ser Gly Ser Gly Gln Gln Ser Val Thr Gly Val Glu Ala Ser
65 70 75

Asp Asp Ala Asn Ser Tyr Trp Arg Ile Arg Gly Gly Ser Glu Gly
80 85 90

Gly Cys Pro Arg Gly Ser Pro Val Arg Cys Gly Gln Ala Val Arg
95 100 105

Leu Thr His Val Leu Thr Gly Lys Asn Leu His Thr His His Phe
110 115 120

Pro Ser Pro Leu Ser Asn Asn Gln Glu Val Ser Ala Phe Gly Glu
125 130 135

Asp Gly Glu Gly Asp Asp Leu Asp Leu Trp Thr Val Arg Cys Ser
140 145 150

Gly Gln His Trp Glu Arg Glu Ala Ala Val Arg Phe Gln His Val
155 160 165

Gly Thr Ser Val Phe Leu Ser Val Thr Gly Glu Gln Tyr Gly Ser
170 175 180

Pro Ile Arg Gly Gln His Glu Val His Gly Met Pro Ser Ala Asn
185 190 195

Thr His Asn Thr Trp Lys Ala Met Glu Gly Ile Phe Ile Lys Pro
200 205 210

Ser Val Glu Pro Ser Ala Gly His Asp Glu Leu
215 220

<210> 75
<211> 1049
<212> DNA
<213> Homo Sapien

<400> 75
gttgctatgt tgcccaggct ggtcttgaag tgccttgacc tcctaaagtg 50

ttggaaccac agacgtgagc cactccaccc agcctaaaac ttcatcttct 100

ttggatgaga tgaacacttt taacaagaga acaggactct atataaatcg 150

ctgtgggctc accacctcta aggaggagca ctgactgaag acagaaaaat 200

tgatgaactg aagaagacat ggtccattat gccttacaaa cttacacagt 250

gctttgggaa ttccaaagta ctcagtggag agaggtgttt caggagccgt 300

agagccagat cgtcatcatg tctgcattgt ggctgctgct gggcctcctt 350

gccctgatgg acttgtctga aagcagcaac tggggatgct atggaaacat 400

ccaaagcctg gacacccctg gagcatcttg tgggattgga agacgtcacg 450

gcctgaacta ctgtggagtt cgtgcttctg aaaggctggc tgaaatagac 500

atgccatacc tcctgaaata tcaacccatg atgcaaacca ttggccaaaa 550

gtactgcatg gatcctgccg tgatcgctgg tgtcttgtcc aggaagtctc 600

ccggtgacaa aattctggtc aacatgggcg ataggactag catggtgcag 650

gaccctggct ctcaagctcc cacatcctgg attagtgagt ctcaggtttc 700

ccagacaact gaagttctga ctactagaat caaagaaatc cagaggaggt 750

ttccaacctg gacccctgac cagtacctga gaggtggact ctgtgcctac 800

agtgggggtg ctggctatgt ccgaagcagc caggacctga gctgtgactt 850

ctgcaatgat gtccttgcac gagccaagta cctcaagaga catggcttct 900

aacatctcag atgaaaccca agaccatgat cacatatgca gcctcaaatg 950

ttacacagat aaaactagcc aagggcacct gtaactggga atctgagttt 1000

gacctaaaag tcattaaaat aacatgaatc ccattaaaaa aaaaaaaaa 1049

<210> 76
<211> 194
<212> PRT
<213> Homo Sapien

<400> 76
Met Ser Ala Leu Trp Leu Leu Leu Gly Leu Leu Ala Leu Met Asp
1 5 10 15

Leu Ser Glu Ser Ser Asn Trp Gly Cys Tyr Gly Asn Ile Gln Ser
20 25 30

Leu Asp Thr Pro Gly Ala Ser Cys Gly Ile Gly Arg Arg His Gly
35 40 45

Leu Asn Tyr Cys Gly Val Arg Ala Ser Glu Arg Leu Ala Glu Ile
50 55 60

Asp Met Pro Tyr Leu Leu Lys Tyr Gln Pro Met Met Gln Thr Ile
65 70 75

Gly Gln Lys Tyr Cys Met Asp Pro Ala Val Ile Ala Gly Val Leu
80 85 90

Ser Arg Lys Ser Pro Gly Asp Lys Ile Leu Val Asn Met Gly Asp
95 100 105

Arg Thr Ser Met Val Gln Asp Pro Gly Ser Gln Ala Pro Thr Ser
110 115 120

Trp Ile Ser Glu Ser Gln Val Ser Gln Thr Thr Glu Val Leu Thr
125 130 135

Thr Arg Ile Lys Glu Ile Gln Arg Arg Phe Pro Thr Trp Thr Pro
140 145 150

Asp Gln Tyr Leu Arg Gly Gly Leu Cys Ala Tyr Ser Gly Gly Ala
155 160 165

Gly Tyr Val Arg Ser Ser Gln Asp Leu Ser Cys Asp Phe Cys Asn
170 175 180

Asp Val Leu Ala Arg Ala Lys Tyr Leu Lys Arg His Gly Phe
185 190

<210> 77
<211> 899
<212> DNA
<213> Homo Sapien

<400> 77
ttgaaaatct actctatcag ctgctgtggt tgccaccatt ctcaggaccc 50

tcgccatgaa agcccttatg ctgctcaccc tgtctgttct gctctgctgg 100

gtctcagctg acattcgctg tcactcctgc tacaaggtcc ctgtgctggg 150

ctgtgtggac cggcagtcct gccgcctgga gccaggacag caatgcctga 200

caacacatgc ataccttggt aagatgtggg ttttctccaa tctgcgctgt 250

ggcacaccag aagagccctg tcaggaggcc ttcaaccaaa ccaaccgcaa 300

gctgggtctg acatataaca ccacctgctg caacaaggac aactgcaaca 350

gcgcaggacc ccggcccact ccagccctgg gccttgtctt ccttacctcc 400

ttggctggcc ttggcctctg gctgctgcac tgagactcat tccattggct 450

gcccctcctc ccacctgcct tggcctgagc ctctctccct gtgtctctgt 500

atcccctggc tttacagaat cgtctctccc tagctcccat ttctttaatt 550

aaacactgtt ccgagtggtc tcctcatcca tccttcccac ctcacaccct 600

tcactctcct ttttctgggt cccttcccac ttccttccag gacctccatt 650

ggctcctaga agggctcccc actttgcttc ctatactctg ctgtccccta 700

cttgaggagg gattgggatc tgggcctgaa atggggcttc tgtgttgtcc 750

ccagtgaagg ctcccacaag gacctgatga cctcactgta cagagctgac 800

tccccaaacc caggctccca tatgtacccc atcccccata ctcacctctt 850

tccattttga gtaataaatg tctgagtctg gaaaaaaaaa aaaaaaaaa 899

<210> 78
<211> 125
<212> PRT
<213> Homo Sapien

<400> 78
Met Lys Ala Leu Met Leu Leu Thr Leu Ser Val Leu Leu Cys Trp
1 5 10 15

Val Ser Ala Asp Ile Arg Cys His Ser Cys Tyr Lys Val Pro Val
20 25 30

Leu Gly Cys Val Asp Arg Gln Ser Cys Arg Leu Glu Pro Gly Gln
35 40 45

Gln Cys Leu Thr Thr His Ala Tyr Leu Gly Lys Met Trp Val Phe
50 55 60

Ser Asn Leu Arg Cys Gly Thr Pro Glu Glu Pro Cys Gln Glu Ala
65 70 75

Phe Asn Gln Thr Asn Arg Lys Leu Gly Leu Thr Tyr Asn Thr Thr
80 85 90

Cys Cys Asn Lys Asp Asn Cys Asn Ser Ala Gly Pro Arg Pro Thr
95 100 105

Pro Ala Leu Gly Leu Val Phe Leu Thr Ser Leu Ala Gly Leu Gly
110 115 120

Leu Trp Leu Leu His
125

<210> 79

<211> 1977
<212> DNA
<213> Homo Sapien

<400> 79
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tgcagctctg cagtcgggcc gttccttcgc cgccgccagg ggtagcggtg 100

tagctgcgca gcgtcgcgcg cgctaccgca cccaggttcg gcccgtaggc 150

gtctggcagc ccggcgccat cttcatcgag cgccatggcc gcagcctgcg 200

ggccgggagc ggccgggtac tgcttgctcc tcggcttgca tttgtttctg 250

ctgaccgcgg gccctgccct gggctggaac gaccctgaca gaatgttgct 300

gcgggatgta aaagctctta ccctccacta tgaccgctat accacctccc 350

gcaggctgga tcccatccca cagttgaaat gtgttggagg cacagctggt 400

tgtgattctt ataccccaaa agtcatacag tgtcagaaca aaggctggga 450

tgggtatgat gtacagtggg aatgtaagac ggacttagat attgcataca 500

aatttggaaa aactgtggtg agctgtgaag gctatgagtc ctctgaagac 550

cagtatgtac taagaggttc ttgtggcttg gagtataatt tagattatac 600

agaacttggc ctgcagaaac tgaaggagtc tggaaagcag cacggctttg 650

cctctttctc tgattattat tataagtggt cctcggcgga ttcctgtaac 700

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ataaagtaga aagttggagt caaacactgg atgcagaaat tttggatttt 1250

tcatcacttt ctctttagaa aaaaagtact acctgttaac aattgggaaa 1300

aggggatatt caaaagttct gtggtgttat gtccagtgta gctttttgta 1350

ttctattatt tgaggctaaa agttgatgtg tgacaaaata cttatgtgtt 1400

gtatgtcagt gtaacatgca gatgtatatt gcagtttttg aaagtgatca 1450

ttactgtgga atgctaaaaa tacattaatt tctaaaacct gtgatgccct 1500

aagaagcatt aagaatgaag gtgttgtact aatagaaact aagtacagaa 1550

aatttcagtt ttaggtggtt gtagctgatg agttattacc tcatagagac 1600

tataatattc tatttggtat tatattattt gatgtttgct gttcttcaaa 1650

catttaaatc aagctttgga ctaattatgc taatttgtga gttctgatca 1700

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gtaactgaat attaccttct gtaggaaaag gtggaaaata agcatctaga 1800

aggttgttgt gaatgactct gtgctggcaa aaatgcttga aacctctata 1850

tttctttcgt tcataagagg taaaggtcaa atttttcaac aaaagtcttt 1900

taataacaaa agcatgcagt tctctgtgaa atctcaaata ttgttgtaat 1950

agtctgtttc aatcttaaaa agaatca 1977

<210> 80
<211> 339
<212> PRT
<213> Homo Sapien

<400> 80

Met	Ala	Ala	Ala	Cys	Gly	Pro	Gly	Ala	Ala	Gly	Tyr	Cys	Leu	Leu	
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Leu	Gly	Leu	His	Leu	Phe	Leu	Leu	Thr	Ala	Gly	Pro	Ala	Leu	Gly	
			20					25						30	
Trp	Asn	Asp	Pro	Asp	Arg	Met	Leu	Leu	Arg	Asp	Val	Lys	Ala	Leu	
			35					40						45	
Thr	Leu	His	Tyr	Asp	Arg	Tyr	Thr	Thr	Ser	Arg	Arg	Leu	Asp	Pro	
			50					55						60	
Ile	Pro	Gln	Leu	Lys	Cys	Val	Gly	Gly	Thr	Ala	Gly	Cys	Asp	Ser	
			65					70						75	
Tyr	Thr	Pro	Lys	Val	Ile	Gln	Cys	Gln	Asn	Lys	Gly	Trp	Asp	Gly	
			80					85						90	
Tyr	Asp	Val	Gln	Trp	Glu	Cys	Lys	Thr	Asp	Leu	Asp	Ile	Ala	Tyr	
			95					100						105	
Lys	Phe	Gly	Lys	Thr	Val	Val	Ser	Cys	Glu	Gly	Tyr	Glu	Ser	Ser	
			110					115						120	
Glu	Asp	Gln	Tyr	Val	Leu	Arg	Gly	Ser	Cys	Gly	Leu	Glu	Tyr	Asn	
			125					130						135	

Leu Asp Tyr Thr Glu Leu Gly Leu Gln Lys Leu Lys Glu Ser Gly
140 145 150

Lys Gln His Gly Phe Ala Ser Phe Ser Asp Tyr Tyr Tyr Lys Trp
155 160 165

Ser Ser Ala Asp Ser Cys Asn Met Ser Gly Leu Ile Thr Ile Val
170 175 180

Val Leu Leu Gly Ile Ala Phe Val Val Tyr Lys Leu Phe Leu Ser
185 190 195

Asp Gly Gln Tyr Ser Pro Pro Pro Tyr Ser Glu Tyr Pro Pro Phe
200 205 210

Ser His Arg Tyr Gln Arg Phe Thr Asn Ser Ala Gly Pro Pro Pro
215 220 225

Pro Gly Phe Lys Ser Glu Phe Thr Gly Pro Gln Asn Thr Gly His
230 235 240

Gly Ala Thr Ser Gly Phe Gly Ser Ala Phe Thr Gly Gln Gln Gly
245 250 255

Tyr Glu Asn Ser Gly Pro Gly Phe Trp Thr Gly Leu Gly Thr Gly
260 265 270

Gly Ile Leu Gly Tyr Leu Phe Gly Ser Asn Arg Ala Ala Thr Pro
275 280 285

Phe Ser Asp Ser Trp Tyr Tyr Pro Ser Tyr Pro Pro Ser Tyr Pro
290 295 300

Gly Thr Trp Asn Arg Ala Tyr Ser Pro Leu His Gly Gly Ser Gly
305 310 315

Ser Tyr Ser Val Cys Ser Asn Ser Asp Thr Lys Thr Arg Thr Ala
320 325 330

Ser Gly Tyr Gly Gly Thr Arg Arg Arg
335